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OM protein - protein search, using sw model

Run on: October 22, 2004, 08:38:11 ; Search time 195 Seconds
(without alignments)
436.695 Million cell updates/sec

Title: US-10-723-368-2

Perfect score: 794

Sequence: 1 MARIPTAALGICSLICQLP.....GPAGRQDSAPVDPSPSHYG 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	794	100.0	148	1	ADM2 HUMAN
2	455	57.3	150	1	ADM2 MOUSE
3	451	56.8	146	1	ADM2 RAT
4	451	56.8	146	1	ADM201302
5	219.5	27.6	168	2	Q75XW7
6	219.5	27.6	168	2	BAD02342
7	204	25.7	159	2	Q75XW6
8	204	25.7	159	2	BAD02343
9	201	25.3	140	2	Q6IFS9
10	99	12.5	186	2	Q8NF75
11	98.5	12.4	953	2	Q6K769
12	98.5	12.4	953	2	BAD21873
13	98.5	12.4	953	2	BAD21878
14	98	12.3	123	2	Q75XW4
15	98	12.3	123	2	BAD02345
16	98	12.3	1458	2	Q6BJT8
17	98	12.3	2715	1	MLLA4 HUMAN
18	97.5	12.3	292	2	Q6GRY6
19	97.5	12.3	1003	1	MBD56 HUMAN
20	97.5	12.3	1003	2	Q6P0P0
21	97.5	12.3	1003	2	AAH65530
22	97	12.2	174	2	Q75XW8
23	97	12.2	174	2	BAD02341
24	96.5	12.2	571	2	Q8NBL0
25	96.5	12.2	1186	1	Q7T401
26	96	12.1	406	1	PG22 HUMAN
27	96	12.1	406	2	BAC03877
28	96	12.1	437	2	Q6Z8R8
29	96	12.1	437	2	BAD10031
30	95.5	12.0	294	2	Q86TW3
31	95.5	12.0	328	2	Q86TQ7

ID	ADM2_HUMAN	STANDARD	PRT	148 AA
AC	Q7Z4H4			
DT	05-JUL-2004	(Rel. 44, Created)		
DT	05-JUL-2004	(Rel. 45, Last sequence update)		
DT	01-OCT-2004	(Rel. 45, Last annotation update)		
DE	Adrenomedullin 2 precursor (Intermedin) [Contains: Adrenomedullin 2 (Intermedin-long) (IMDL); Intermedin-short (IMDS)].			
GN	Name=ADM2; Synonyms=AM2;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.			
RX	PubMed=14615490; DOI=10.1016/j.jbc.2003.03.020;			
RA	Roh J., Chang C.D., Bhalla A., Klein C., Hsu S.Y.T.;			
RT	"Intermedin is a calcitonin/calcitonin gene-related peptide family			
RT	peptide acting through the calcitonin receptor-like receptor/receptor			
RT	activity-modifying protein receptor complexes.";			
RL	J. Biol. Chem. 279:7264-7274(2004).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1;			
RA	Takei Y., Inoue K., Ogoshi M., Kawahara T., Bannai H., Miyano S.;			
RT	"Identification of novel adrenomedullin in mammals: a potent			
RT	cardiovascular and renal regulator.";			
RL	FEBS Lett. 556:53-58(2004).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;			
RA	Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,			
RA	Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,			
RA	Bagdugley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,			
RA	Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,			
RA	Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,			
RA	Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,			
RA	Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,			
RA	Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,			
RA	Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,			
RA	Gilbert J.G.R., Goward M.E., Grafton D.V., Griffiths M.N.D., Hall C.,			
RA	Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,			
RA	Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,			
RA	Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,			
RA	Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,			
RA	Mcclay J.C., McMurphy A.A., Milne S.A., Mortimore B.J.,			
RA	Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,			
RA	Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,			
RA	Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,			
RA	Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,			
RA	Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,			
RA	Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilting L.,			

ALIGNMENTS

ADM2_HUMAN	STANDARD	PRT	148 AA
32	95.5	12.0	414
33	95.5	12.0	414
34	95.5	12.0	571
35	95	12.0	1829
36	95	12.0	1832
37	94.5	11.9	201
38	94	11.8	155
39	94	11.8	171
40	94	11.8	171
41	94	11.8	756
42	93.5	11.8	414
43	93.5	11.8	619
44	93	11.7	216
45	93	11.7	500

Q6mlw2	corynebacte
CaF20925	corynebacte
Q6h9l7	homo sapien
O15015	homo sapien
Q8lvd8	homo sapien
Q9haa0	homo sapien
Q9pcsl	xanthomonas
Q6l8k5	cyprinus ca
Bad19046	cyprinus
Q6c2z4	yarrowia li
Q9eeez	arabidopsis
Q8zll8	streptomyce
Q80va6	mus musculu
Q99526	homo sapien

RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudo J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuayama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chiesse S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Benis G., Bentley J., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozerky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L., Wardis E., Waterston R., Wilson R.,
RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
RA Srour E., Franssen I., Tapia I., Bruder C.B., O'Brien K.P.,
RA Wilkison P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tiliakou Y., Wright H.;
RA "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
CC -i- FUNCTION: IMDL and IMDS may play a role as physiological
CC regulators of gastrointestinal, cardiovascular bioactivities
CC mediated by the CALCR1/RAMPs receptor complexes. Activates the
CC CAMP-dependent pathway.
CC -i- SUBCELLULAR LOCATION: Secreted.
CC -i- TISSUE SPECIFICITY: Expressed in the esophagus, stomach, jejunum,
CC ileum, ileocecum, ascending colon, transverse colon, descending
CC colon and rectum.
CC -i- SIMILARITY: Belongs to the adrenomedullin family.
CC -----
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CC -----
CC EMBL; AF529213; AAC09100.1; -;
CC EMBL; AB121034; BAD07411.1; -;
CC EMBL; AL096767; -; NOT_ANNOTATED_CDS.
CC Genew; HGNC:28898; ADM2.
CC MIM; 608682; -;
CC -----
CC Amidation; Cleavage on pair of basic residues; Hormone; Signal.
CC SIGNAL 1 24 Potential.
CC PROPEP 25 98 By similarity.
CC PEPTIDE 101 147 Adrenomedullin 2 (By similarity).
CC PEPTIDE 108 147 Intermedin-short (Potential).
CC DISULFID 110 115 By similarity.
CC MOD_RES 147 147 Tyrosine amide (G-148 provides amide
CC group) (Probable).
CC SEQUENCE 148 AA; 15865 MW; 5E0E3098CFCE5BE2 CRC64;
CC -----
CC Query Match 100.0%; Score 794; DB 1; Length 148;
CC Best Local Similarity 100.0%; Pred. No. 2.2e-52;
CC Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC 1 MARIPAAAGCISLLCLQPLGSLSRSLGDPVPKPEPPARSPSSSLQPRHPAPRVVW 60
CC |||||
CC 1 MARIPAAAGCISLLCLQPLGSLSRSLGDPVPKPEPPARSPSSSLQPRHPAPRVVW 60
CC |||||
CC 61 KLHRAQAQAGAGLAPVWGQPLRDGGHSGPRRHSGPRRTQALLRVGCVLGTCCQVNL 120
CC |||||
CC 61 KLHRAQAQAGAGLAPVWGQPLRDGGHSGPRRHSGPRRTQALLRVGCVLGTCCQVNL 120
CC |||||
CC 121 SHRLWQLMGAGAQDSAPVDPSPSPHSYG 148
CC |||||
CC 121 SHRLWQLMGAGAQDSAPVDPSPSPHSYG 148
CC |||||

RESULT 2

ADM2 MOUSE
ID ADM2_MOUSE STANDARD; PRT; 150 AA.
AC Q7TNK8;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Adrenomedullin 2 precursor (Intermedin) [Contains: Adrenomedullin 2
DE (Intermedin-long) (IMDL); Intermedin-short (IMDS)].
OS Name:Adm2; Synonyms:Am2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC STRAIN=C57BL/6;
RC PubMed=14615490; DOI=10.1074/jbc.M305332200;
RX Roh J., Chang C.L., Bhalla A., Klein C., Hsu S.Y.T.;
RA "Intermedin is a calcitonin/calcitonin gene-related peptide family
RA peptide acting through the calcitonin receptor-like receptor/receptor
RA activity-modifying protein receptor complexes.";
RL J. Biol. Chem. 279:7264-7274(2004).
RN [2]
RN SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Kidney;
RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1;
RA Takei Y., Inoue K., Ogoshi M., Kawahara T., Bannai H., Miyano S.;
RA "Identification of novel adrenomedullin in mammals: a potent
RA cardiovascular and renal regulator.";
RL FEBS Lett. 556:53-58(2004).
CC -i- FUNCTION: IMDL and IMDS may play a role as physiological
CC regulators of gastrointestinal, cardiovascular bioactivities
CC mediated by the CALCR1/RAMPs receptor complexes. Activates the
CC CAMP-dependent pathway.
CC -i- SUBCELLULAR LOCATION: Secreted.
CC -i- TISSUE SPECIFICITY: High expression detected in the submaxillary
CC gland, kidney, stomach, and mesentery, followed by the pituitary,
CC lung, pancreas, intestines, spleen, thymus and ovary. Expressed
CC mainly in the intermediate lobe of the pituitary, with sporadic in
CC the anterior lobe.
CC -i- SIMILARITY: Belongs to the adrenomedullin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF529212; AAC09099.1; -;
CC EMBL; AB121035; BAD07412.1; -;
CC MGD; MGI:2675256; Adm2.
CC Amidation; Cleavage on pair of basic residues; Hormone; Signal.
CC SIGNAL 1 25 Potential.
CC PROPEP 26 100 By similarity.
CC PEPTIDE 103 149 Adrenomedullin 2 (By similarity).
CC PEPTIDE 110 149 Intermedin-short (Potential).
CC DISULFID 112 117 By similarity.
CC MOD_RES 149 149 Tyrosine amide (G-150 provides amide
CC group) (Probable).
CC SEQUENCE 150 AA; 16188 MW; 2BFF392BFBFBBA CRC64;
CC -----
CC Query Match 57.3%; Score 455; DB 1; Length 150;
CC Best Local Similarity 66.0%; Pred. No. 7.2e-27;
CC Matches 95; Conservative 12; Mismatches 35; Indels 2; Gaps 2;
CC -----
CC 6 TAAAGCISLLCLQPLGSLSRSLGDPVPKPEPPARSPSSSLQPRHPAPRVVWKLHR- 64
CC |||||
CC 8 TATLGCISLLYL-LPGTSLGSLGKLRHSRPREPPAKIPSSNLQPGHPSLQPVVWKKRRH 66
CC |||||
CC 65 ALQAQAGAGLAPVWGQPLRDGGHSGPRRHSGPRRTQALLRVGCVLGTCCQVNLSHRL 124
CC |||||

```

Db 67 APQPQGRGNRLAMVHLFQGGSRHPGQRTGTSGRRPAPHAQLLRVGCVLGTCQVQNLSHRL 126
QY 125 WOLMGPAQRODSAPVDPSPSPHSYG 148
Db 127 WOLVPSGRDSDAPVDPSPSPHSYG 150

RESULT 3
ADM2_RAT
ID ADM2_RAT STANDARD; PRT; 146 AA.
AC P61312;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Adrenomedullin 2 precursor (Intermedin) [Contains: Adrenomedullin 2
DE (Intermedin-long) (IMDL); Intermedin-short (IMDS)].
GN Name=Adm2; Synonyms=Am2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1;
RA Takei Y., Inoue K., Ogoshi M., Kawahara T., Bannai H., Miyano S.;
RT "Identification of novel adrenomedullin in mammals: a potent
RT cardiovascular and renal regulator.";
RL FEBS Lett. 556:53-58(2004).
RN [2]
RP FUNCTION, AND TISSUE SPECIFICITY.
RX PubMed=14615490; DOI=10.1074/jbc.M305332200;
RA Roh J., Chang C.L., Bhalla A., Klein C., Hsu S.Y.T.;
RT "Intermedin is a calcitonin/calcitonin gene-related peptide family
RT peptide acting through the calcitonin receptor-like receptor/receptor
RT activity-modifying protein receptor complexes.";
RL J. Biol. Chem. 279:7264-7274(2004).
CC -!- FUNCTION: IMDL and IMDS may play a role as physiological
CC regulators of gastrointestinal, cardiovascular bioactivities
CC mediated by the CALCRL/RAMPs receptor complexes. Activates the
CC CAMP-dependent pathway.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expression was restricted to the intermediate
CC and anterior lobes of the pituitary.
CC -!- SIMILARITY: Belongs to the adrenomedullin family.
CC
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CC
DR EMBL; AB121036; BAD07413.1; -.
KW Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 96 By similarity.
FT PEPTIDE 99 145 Adrenomedullin 2 (By similarity).
FT PEPTIDE 106 145 Intermedin-short (Potential).
FT DISULFID 108 113 By similarity.
FT MOD_RES 145 145 Tyrosine amide (G-146 provides amide
FT group) (Probable).
FT SEQUENCE 146 AA; 15572 MW; C87043237AD29DDC CRC64;

Query Match 56.8%; Score 451; DB 1; Length 146;
Best Local Similarity 65.3%; Pred. No. 1.4e-26;
Matches 94; Conservative 13; Mismatches 31; Indels 6; Gaps 4;

Kw Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 96 By similarity.
FT PEPTIDE 99 145 Adrenomedullin 2 (By similarity).
FT PEPTIDE 106 145 Intermedin-short (Potential).
FT DISULFID 108 113 By similarity.
FT MOD_RES 145 145 Tyrosine amide (G-146 provides amide
FT group) (Probable).
FT SEQUENCE 146 AA; 15572 MW; C87043237AD29DDC CRC64;

Query Match 56.8%; Score 451; DB 1; Length 146;
Best Local Similarity 65.3%; Pred. No. 1.4e-26;
Matches 94; Conservative 13; Mismatches 31; Indels 6; Gaps 4;

QY 6 TAAAGCISILCLQPGSLRSISGGDPKPRPVKPREPPARSPSSSLQPHAPRPVWVKLHRA 65
Db 8 TWTFCISILLYL-LPGTLSSGLG---KGLRPREPPAKIPSSGPGQGHPSLRPVWVKPPHA 63

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QY 66 LQAO-RGAGLAPVMGQPLRDGGRHSGRRRSPRTQAQLLRVGCVLGTCQVQNLSHRL 124
Db 64 LQPGQGRGNPALATVHLP-QGGSRHPGQRTGTSGRRPAPHAQLLRVGCVLGTCQVQNLSHRL 122
QY 125 WOLMGPAQRODSAPVDPSPSPHSYG 148
Db 123 WOLVPSGRDSDAPVDPSPSPHSYG 146

RESULT 4
AAT01302
ID AAT01302 PRELIMINARY; PRT; 146 AA.
AC AAT01302;
DT 10-MAY-2004 (TREMELrel. 27, Created)
DT 10-MAY-2004 (TREMELrel. 27, Last sequence update)
DE Adrenomedullin 2 precursor (Intermedin) [Contains: Adrenomedullin 2
DE (Intermedin-long) (IMDL); Intermedin-short (IMDS)].
GN Name=Adm2; Synonyms=Am2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Chang C.L., Roh J., Hsu S.Y.;
RT "Rat IMD sequence.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY590103; AAT01302.1; -.
SQ SEQUENCE 146 AA; 15572 MW; C87043237AD29DDC CRC64;

Query Match 56.8%; Score 451; DB 2; Length 146;
Best Local Similarity 65.3%; Pred. No. 1.4e-26;
Matches 94; Conservative 13; Mismatches 31; Indels 6; Gaps 4;

QY 6 TAAAGCISILCLQPGSLRSISGGDPKPRPVKPREPPARSPSSSLQPHAPRPVWVKLHRA 65
Db 8 TWTFCISILLYL-LPGTLSSGLG---KGLRPREPPAKIPSSGPGQGHPSLRPVWVKPPHA 63
QY 66 LQAO-RGAGLAPVMGQPLRDGGRHSGRRRSPRTQAQLLRVGCVLGTCQVQNLSHRL 124
Db 64 LQPGQGRGNPALATVHLP-QGGSRHPGQRTGTSGRRPAPHAQLLRVGCVLGTCQVQNLSHRL 122
QY 125 WOLMGPAQRODSAPVDPSPSPHSYG 148
Db 123 WOLVPSGRDSDAPVDPSPSPHSYG 146

RESULT 5
Q75XW7
ID Q75XW7 PRELIMINARY; PRT; 168 AA.
AC Q75XW7;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DE Adrenomedullin-2.
GN Name=ADM2;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphii; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22984567; PubMed=14623291;
RA Ogoshi M., Inoue K., Takei Y.;
RT "Identification of a novel adrenomedullin gene family in teleost
RT fish.";
RL Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
DR EMBL; AB120296; BAD02342.1; -.
SQ SEQUENCE 168 AA; 18544 MW; A5905E7CC112669B CRC64;

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Query Match 27.6%; Score 219.5; DB 2; Length 168;
Best Local Similarity 41.1%; Pred. No. 4.2e-09;
Matches 67; Conservative 21; Mismatches 44; Indels 31; Gaps 10;

QY 12 ISLLCLQPG-SLSRSLGGP-----RPVK-PREP-----PARSPSSSLQPRHPARP- 57
DB 11 LSLLPLEVQARALSQQNLGPHRFSLLRTLKIPKSSFIVIGPAASDPPEVYHHVAQGDG 70
QY 58 -VVMKHLRALQAQRAGLA----PVMGQP---LRD--GGRQHSQPRRH--SGPRRTQAOL 105
DB 71 RVTW-----MAWLRGKPLLGSSDPLQGTDRVLRDTPAWGRSGRGRHANNGGSRHGQL 125
QY 106 LRVGCVLTGTCQVONLSHRLWLMGPAGRODSAPVDPSPSPHSYG 148
DB 126 MRVACVLGTQCVONLSHRLYQLIQSGKEDSSPMNPHSPHSYG 168

RESULT 6
BAD02342 PRELIMINARY; PRT; 168 AA.
ID BAD02342; AC BAD02342;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE Adrenomedullin-2.
GN ADM2.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP MEDLINE=22984567; PubMed=14623291;
RA Ogoshi M., Inoue K., Takei Y.;
RT "Identification of a novel adrenomedullin gene family in teleost fish."
RL Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
DR EMBL; AB120296; BAD02342.1; -.
SQ SEQUENCE 168 AA; 18544 MW; A5905E7CC112669B CRC64;

Query Match 27.6%; Score 219.5; DB 2; Length 168;
Best Local Similarity 41.1%; Pred. No. 4.2e-09;
Matches 67; Conservative 21; Mismatches 44; Indels 31; Gaps 10;

QY 12 ISLLCLQPG-SLSRSLGGP-----RPVK-PREP-----PARSPSSSLQPRHPARP- 57
DB 11 LSLLPLEVQARALSQQNLGPHRFSLLRTLKIPKSSFIVIGPAASDPPEVYHHVAQGDG 70
QY 58 -VVMKHLRALQAQRAGLA----PVMGQP---LRD--GGRQHSQPRRH--SGPRRTQAOL 105
DB 71 RVTW-----MAWLRGKPLLGSSDPLQGTDRVLRDTPAWGRSGRGRHANNGGSRHGQL 125
QY 106 LRVGCVLTGTCQVONLSHRLWLMGPAGRODSAPVDPSPSPHSYG 148
DB 126 MRVACVLGTQCVONLSHRLYQLIQSGKEDSSPMNPHSPHSYG 168

RESULT 7
Q75XW6 PRELIMINARY; PRT; 159 AA.
ID Q75XW6; AC Q75XW6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Adrenomedullin-3.
GN Name=ADM3;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.

OX NCBI_TaxID=31033;
RN [1]
RP MEDLINE=22984567; PubMed=14623291;
RA Ogoshi M., Inoue K., Takei Y.;
RT "Identification of a novel adrenomedullin gene family in teleost fish."
RL Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
DR EMBL; AB120297; BAD02343.1; -.
SQ SEQUENCE 159 AA; 18028 MW; F1863B20100E254D CRC64;

Query Match 25.7%; Score 204; DB 2; Length 159;
Best Local Similarity 34.8%; Pred. No. 5.8e-08;
Matches 62; Conservative 16; Mismatches 32; Indels 68; Gaps 9;

QY 11 CISLLCL-----QLP-----GSLRSILGG-DPRPVKPREPPARSPS 45
DB 10 CISLLSFRLLETLPABELPDENRLDDIIDQRDKSSVSRQKNIDVPL-----A 59
QY 46 SSLQPR-----HPAPRPVVMKL-----HRLAQRGAGLAPVVMQPLRDGGRHS- 90
DB 60 SSLSPKWLKSHSGIHSGVKVLRSLAWARPQRRLFRARR-----HIHSR 103
QY 91 GPRHSGPRRTQAQLRVGCVLTGTCQVONLSHRLWLMGPAGRODSAPVDPSPSPHSYG 148
DB 104 GMRGHYPHPN--QLIRAGCALGTQCVONLSHRLYQLIQSGRDDSSPINPKSPHSYG 159

RESULT 8
BAD02343 PRELIMINARY; PRT; 159 AA.
ID BAD02343; AC BAD02343;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE Adrenomedullin-3.
GN ADM3.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP MEDLINE=22984567; PubMed=14623291;
RA Ogoshi M., Inoue K., Takei Y.;
RT "Identification of a novel adrenomedullin gene family in teleost fish."
RL Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
DR EMBL; AB120297; BAD02343.1; -.
SQ SEQUENCE 159 AA; 18028 MW; F1863B20100E254D CRC64;

Query Match 25.7%; Score 204; DB 2; Length 159;
Best Local Similarity 34.8%; Pred. No. 5.8e-08;
Matches 62; Conservative 16; Mismatches 32; Indels 68; Gaps 9;

QY 11 CISLLCL-----QLP-----GSLRSILGG-DPRPVKPREPPARSPS 45
DB 10 CISLLSFRLLETLPABELPDENRLDDIIDQRDKSSVSRQKNIDVPL-----A 59
QY 46 SSLQPR-----HPAPRPVVMKL-----HRLAQRGAGLAPVVMQPLRDGGRHS- 90
DB 60 SSLSPKWLKSHSGIHSGVKVLRSLAWARPQRRLFRARR-----HIHSR 103
QY 91 GPRHSGPRRTQAQLRVGCVLTGTCQVONLSHRLWLMGPAGRODSAPVDPSPSPHSYG 148
DB 104 GMRGHYPHPN--QLIRAGCALGTQCVONLSHRLYQLIQSGRDDSSPINPKSPHSYG 159

RESULT 9
Q6IFS9 PRELIMINARY; PRT; 140 AA.

122 PLYLTHSPFLRHQSTQAVPAPHLSYQIWEGDDMKTTQPLSRRS-----GVC--RGADRLWK 177

127 LMG-PAG 132
| | | | |

177 LQGLPAG 183

RESULT 11

Q6K769 PRELIMINARY; PRT; 953 AA.

ID Q6K769; AC Q6K769;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 01-OCT-2004 (TrEMBLrel. 26, Last annotation update)

DE Putative O-linked N-acetyl glucosamine transferase.

GN Name=OSJNBa048K16.5; Synonyms=P0483C08.45;

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.

ON NCBI_TaxID=39947;

OX [1]

SEQUENCE FROM N.A.

RA Sasaki T., Matsumoto T., Yamamoto K.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP004864; BAD21878.1; -

DR EMBL; AP004837; BAD21873.1; -

GO; GO:0016740; F:transferase activity; IEA.

DR InterPro; IPR001440; TPR.

DR InterPro; IPR008941; TPR-like.

DR Pfam; PF00515; TPR; 13.

DR SMART; SM00028; TPR; 13.

DR PROSITE; PS50005; TPR; 11.

DR PROSITE; PS50293; TPR REGION; 1.

KW Repeat; TPR repeat; Transferase.

SQ SEQUENCE 953 AA; 107236 MW; DECC9A24EACF78EA CRC64;

Query Match 12.4%; Score 98.5; DB 2; Length 953;
Best local similarity 26.4%; Pred. No. 27;
Matches 43; Conservative 16; Mismatches 53; Indels 51; Gaps 8

QY 22 SLSSLSLGGDRPVKPRPPP-----ARSPSSSIQP----- 50

DB 3 SLQQQGGDRPPQPPQAAAPALLGGADWLGFGRAAAELDESVAASFLLPPAPPVDARA 62

QY 51 -RHPAPRPVVMKLRALQAQAGAGLAPVWGQPLRDG----GRQHSQPRRHSGPRRTQAL 105

DB 63 QAQPEPKP---KQLGAVDVERHLA---HQNYSRGKYKEALEHGNIVYEKNPRTD-NL 115

QY 106 LRVCGVLGTQCVQNLSHRLWOLMGPAQGSAPVDPSPHSYG 148

DB 116 LLLGAIY--YQIRNVD-----MCTAKNEEALAIIDNFAECYG 150

RESULT 12

BAD21873 PRELIMINARY; PRT; 953 AA.

ID BAD21873; AC BAD21873;

DT 01-JUN-2004 (TrEMBLrel. 27, Created)

DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)

DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)

DE Putative O-linked N-acetyl glucosamine transferase.

GN P0483C08.45.

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza; Oryza sativa.

ON NCBI_TaxID=39947;

OX [1]

SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare;

RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, PAC

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RT clone:P0483C08.1;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP004837; BAD21873.1; -.
KW Transferase.
SQ SEQUENCE 953 AA; 107236 MW; DECC9A24EACF78EA CRC64;

Query Match 12.4%; Score 98.5; DB 2; Length 953;
Best Local Similarity 26.4%; Pred. No. 27;
Matches 43; Conservative 16; Mismatches 53; Indels 51; Gaps 8;

QY 22 SLRSLSGGDRPVKPREPP-----ARSPSSSLOP----- 50
DB 3 SLOQQGGDRPQPOAAPALLGGADWLGFGRAAELDSVASSPASFLPPAPPVDARA 62

QY 51 -RHAPRPVVKLHRAQAQAGAGLAPVWGQPLRDG---GROHSGPRRHSGPRRTQAO 105
DB 63 QAQPEKPP---KQLGAVDVERHLALA---HQNYSRGYKKEALHGNIVYKKNPRTD-NL 115

QY 106 LRVCVGLGTCQVQNLSHRLWQMGPAQGRDSAPVDPSPSHSYG 148
DB 116 LLLGAIY--YQIRNYD-----MCIKNEEALADPNFAECYG 150

RESULT 13
BAD21878
ID BAD21878 PRELIMINARY; PRT; 953 AA.
AC BAD21878;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative O-linked N-acetyl glucosamine transferase.
GN OSUNBA0048K16.5.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza; Oryza sativa.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC
clone:OSUNBA0048K16.5."
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP004864; BAD21878.1; -.
KW Transferase.
SQ SEQUENCE 953 AA; 107236 MW; DECC9A24EACF78EA CRC64;

Query Match 12.4%; Score 98.5; DB 2; Length 953;
Best Local Similarity 26.4%; Pred. No. 27;
Matches 43; Conservative 16; Mismatches 53; Indels 51; Gaps 8;

QY 22 SLRSLSGGDRPVKPREPP-----ARSPSSSLOP----- 50
DB 3 SLOQQGGDRPQPOAAPALLGGADWLGFGRAAELDSVASSPASFLPPAPPVDARA 62

QY 51 -RHAPRPVVKLHRAQAQAGAGLAPVWGQPLRDG---GROHSGPRRHSGPRRTQAO 105
DB 63 QAQPEKPP---KQLGAVDVERHLALA---HQNYSRGYKKEALHGNIVYKKNPRTD-NL 115

QY 106 LRVCVGLGTCQVQNLSHRLWQMGPAQGRDSAPVDPSPSHSYG 148
DB 116 LLLGAIY--YQIRNYD-----MCIKNEEALADPNFAECYG 150

RESULT 14
Q75XW4
ID Q75XW4 PRELIMINARY; PRT; 123 AA.
AC Q75XW4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Adrenomedullin-5.
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GN Name=ADMS;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22984567; PubMed=14623291;
RA Ogoshi M., Inoue K., Takei Y.;
RT "Identification of a novel adrenomedullin gene family in teleost
fish.";
RL Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
DR EMBL; AB120299; BAD02345.1; -.
SQ SEQUENCE 123 AA; 13538 MW; D3ED4CDBCFC4ECEB CRC64;

Query Match 12.3%; Score 98; DB 2; Length 123;
Best Local Similarity 28.8%; Pred. No. 4.3;
Matches 36; Conservative 10; Mismatches 33; Indels 46; Gaps 6;

QY 50 PRHPAPRPVV-----WKLHRAQAQAGAGLAPV-----MGQPLR 83
DB 18 PLRPTPRDAVLPAQTVQSGSLKTETQAOHAQALRIVPFISEIKNLNLEILKHEMAARLR 77

QY 84 DGRQHSGPRRHSGPRRTQAOQLLRVGCVLGTCQVQNLSHRLWQMGPAQGRDSAPVDPSS 143
DB 78 -----PRR--APQR-----GCQVGTQVHNLANKLYQIGRQGDSTKV--ND 117

QY 144 PHSYG 148
DB 118 PQGYG 122

RESULT 15
BAD02345
ID BAD02345 PRELIMINARY; PRT; 123 AA.
AC BAD02345;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE Adrenomedullin-5.
GN ADMS.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22984567; PubMed=14623291;
RA Ogoshi M., Inoue K., Takei Y.;
RT "Identification of a novel adrenomedullin gene family in teleost
fish.";
RL Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
DR EMBL; AB120299; BAD02345.1; -.
SQ SEQUENCE 123 AA; 13538 MW; D3ED4CDBCFC4ECEB CRC64;

Query Match 12.3%; Score 98; DB 2; Length 123;
Best Local Similarity 28.8%; Pred. No. 4.3;
Matches 36; Conservative 10; Mismatches 33; Indels 46; Gaps 6;

QY 50 PRHPAPRPVV-----WKLHRAQAQAGAGLAPV-----MGQPLR 83
DB 18 PLRPTPRDAVLPAQTVQSGSLKTETQAOHAQALRIVPFISEIKNLNLEILKHEMAARLR 77

QY 84 DGRQHSGPRRHSGPRRTQAOQLLRVGCVLGTCQVQNLSHRLWQMGPAQGRDSAPVDPSS 143
DB 78 -----PRR--APQR-----GCQVGTQVHNLANKLYQIGRQGDSTKV--ND 117

QY 144 PHSYG 148
DB 118 PQGYG 122
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Db 118 PQYG 122

Search completed: October 22, 2004, 08:54:32
Job time : 201 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2004, 08:46:21 ; Search time 40 Seconds
(without alignments)
245.377 Million cell updates/sec

Title: US-10-723-368-2

Perfect score: 794

Sequence: 1 MARIPTAALGICISLLCLQLP.....GPAGRQDSAPVDPSPSHSG 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	110	13.9	379	4	US-09-252-991A-26924	Sequence 26924, A
2	108	13.6	362	4	US-09-252-991A-31641	Sequence 31641, A
3	107.5	13.5	514	4	US-09-252-991A-28208	Sequence 28208, A
4	103.5	13.0	621	4	US-09-252-991A-30689	Sequence 30689, A
5	103	13.0	142	4	US-09-252-991A-21581	Sequence 21581, A
6	102.5	12.9	417	4	US-09-252-991A-24041	Sequence 24041, A
7	101	12.7	327	4	US-09-252-991A-30948	Sequence 30948, A
8	100.5	12.7	528	4	US-09-252-991A-18286	Sequence 18286, A
9	100	12.6	464	4	US-09-252-991A-25833	Sequence 25833, A
10	100	12.6	783	4	US-09-252-991A-18035	Sequence 18035, A
11	99.5	12.5	763	4	US-09-252-991A-30146	Sequence 30146, A
12	99	12.5	373	4	US-09-252-991A-24961	Sequence 24961, A
13	99	12.5	588	4	US-09-252-991A-30690	Sequence 30690, A
14	98.5	12.4	176	4	US-09-252-991A-30542	Sequence 30542, A
15	98.5	12.4	275	4	US-09-252-991A-23976	Sequence 23976, A
16	98.5	12.4	362	4	US-09-252-991A-31016	Sequence 31016, A
17	98.5	12.4	364	4	US-09-252-991A-19923	Sequence 19923, A
18	98.5	12.4	498	4	US-09-252-991A-21973	Sequence 21973, A
19	98.5	12.4	642	4	US-09-252-991A-24767	Sequence 24767, A
20	98.5	12.4	642	4	US-09-252-991A-32104	Sequence 32104, A
21	98	12.3	266	4	US-09-252-991A-30538	Sequence 30538, A
22	97.5	12.3	142	4	US-09-252-991A-16714	Sequence 16714, A
23	97.5	12.3	416	4	US-09-252-991A-24575	Sequence 24575, A
24	97.5	12.3	436	4	US-09-252-991A-31117	Sequence 31117, A
25	97	12.2	317	4	US-09-252-991A-31126	Sequence 31126, A
26	97	12.2	653	4	US-09-252-991A-21418	Sequence 21418, A
27	97	12.2	720	4	US-09-252-991A-31915	Sequence 31915, A

28	96.5	12.2	230	4	US-09-252-991A-28838	Sequence 28838, A
29	96.5	12.2	392	4	US-09-252-991A-31291	Sequence 31291, A
30	96.5	12.2	538	4	US-09-252-991A-21622	Sequence 21622, A
31	96	12.1	260	4	US-09-252-991A-31985	Sequence 31985, A
32	95.5	12.0	315	4	US-09-252-991A-20553	Sequence 20553, A
33	95.5	12.0	457	4	US-09-252-991A-29671	Sequence 29671, A
34	95	12.0	1228	4	US-09-252-991A-17764	Sequence 17764, A
35	94.5	11.9	225	4	US-09-252-991A-25503	Sequence 25503, A
36	94.5	11.9	372	4	US-09-252-991A-23226	Sequence 23226, A
37	94.5	11.9	404	4	US-09-252-991A-21555	Sequence 21555, A
38	94.5	11.9	414	4	US-09-252-991A-27895	Sequence 27895, A
39	94.5	11.9	626	4	US-09-252-991A-27835	Sequence 27835, A
40	94.5	11.9	770	4	US-09-252-991A-28510	Sequence 28510, A
41	94	11.8	193	4	US-09-252-991A-19226	Sequence 19226, A
42	94	11.8	246	4	US-09-252-991A-20289	Sequence 20289, A
43	94	11.8	416	4	US-09-252-991A-17590	Sequence 17590, A
44	94	11.8	489	4	US-09-252-991A-16940	Sequence 16940, A
45	94	11.8	531	4	US-09-252-991A-24404	Sequence 24404, A

ALIGNMENTS

RESULT 1
US-09-252-991A-26924
; Sequence 26924, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26924
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26924

Query Match	13.9%;	Score 110;	DB 4;	Length 379;
Best Local Similarity	29.2%;	Pred. No. 0.0026;		
Matches	50;	Conservative	15;	Mismatches 56; Indels 50; Gaps 8;
QY	4	IPTAALGICISLLC-----LQFGLSRSLGGDF-----RVKPRPPPARSPS	45	
Db	70	LPHVGLGRRLPLAVVGHRRPADRHVHRHLQGTAVRRLQHGFAFPDRAVTRQHPGAARPA	129	
QY	46	SSL-----OPHPAPRPVVKLHRLALQORAGLAPVWGQLRDGGRHSGRRHSG	97	
Db	130	RLVRLRLGREQPPALRLLSAEYHRP-PATTGHIQ-----ROERAPGRHAG	177	
QY	98	PRRTOAQLLRGCVLGTCCVONLSHRLWQLMGPAGRQDSAPVDPSPSHSYG	148	
Db	178	HQRHAG-----DLGRLQORPA-RLPSVAAP-----RHPVDFGLHHPG	216	

RESULT 2
US-09-252-991A-31641
; Sequence 31641, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18

Sequence 30689, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30689
LENGTH: 621
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30689

Query Match 13.0%; Score 103.5; DB 4; Length 621;
Best Local Similarity 28.4%; Pred. No. 0.022;
Matches 40; Conservative 13; Mismatches 45; Indels 43; Gaps 7;
QY 31 PRVVKPREPPARSPSSSLQPRHPAPRVVWKLHRAQAQAGLAPVWGQPLRDGGR--- 87
Db 421 PDPAETQPP-RQWLLAVAFGQRPAPV-----ESRPAHQPALAP--GRPIRRAGALAY 472
QY 88 --QHSGRPHSGPRRTQAQLRVGCVLGTQVQNL--SHELWOL----- 127
Db 473 PEGHGAARRHADPR-----GTAAQORLAASRALRQHASARPAAGNRRRAGD 520
QY 128 MGPAGRQDSAPVDFSPSHSYG 148
Db 521 LPAGRRHRVHAAPAPRATG 541

RESULT 5
US-09-252-991A-21581
Sequence 21581, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21581
LENGTH: 142
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21581

Query Match 13.0%; Score 103; DB 4; Length 142;
Best Local Similarity 39.3%; Pred. No. 0.0043;
Matches 35; Conservative 6; Mismatches 34; Indels 14; Gaps 7;
QY 25 RSLGGDP----RPVKPREPPARSPSSSLQPRH--PAP-RPVWKLHRAQAQOR-GAGLAP 76
Db 11 RTRGGQPAQRRALQPRPP---PGGACQORRLPAPRPRPWARRRRRTAGAVGRAVLP 67
QY 77 VMGQPLRDGGRQHSQ---PRHSGPRRTQA 103
Db 68 -RTQPEQFGTRPGEGHPPRHRAPRAPA 95

RESULT 6

PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31641
LENGTH: 362
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31641

Query Match 13.6%; Score 108; DB 4; Length 362;
Best Local Similarity 32.9%; Pred. No. 0.004;
Matches 50; Conservative 16; Mismatches 42; Indels 44; Gaps 10;
QY 17 LQLPGSLRSR--LGGDPRVVKP-----REP---PARSPSS-- 47
Db 206 LRRLRNLTARRCAGGLFRPAGGQMAARPGRRGAPGQPADWRRAPRCGPRTFVAAR 265
QY 48 --LQPRHPAPRVVWKLHRAQAQAGLAPVWGQPLRDGGRQHSGRPHSGPRRTQAQL 105
Db 266 RDLRPEYGAPRPAIRRRR--RADHGATAA---GGVAGEGQRPASGPRQ---PRRARAQR 317
QY 106 LRVCGLVGTQVQNLHRLWQLMGPAGRQDSA 137
Db 318 ROAGQV-GKDGQPPQSR--LRGP-GRAPGA 344

RESULT 3
US-09-252-991A-28208
Sequence 28208, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28208
LENGTH: 514
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28208

Query Match 13.5%; Score 107.5; DB 4; Length 514;
Best Local Similarity 27.7%; Pred. No. 0.0067;
Matches 54; Conservative 11; Mismatches 51; Indels 79; Gaps 11;
QY 20 PGSLSRL-----GGDPR---PVKPREPPARS-----PSSSLQ-- 50
Db 178 PGRFRFRALPARLOQTAEARRGKPGAAPAGADPRAYFGFPQPWPWRCRALPGGSLRPAG 237
QY 51 -RHAPAPRVVWKLHRAQAQAGLAPVWGQ-----PLRDGGRQH-----SGPR 93
Db 238 EHHQRP-----CRRAPCORPGRVLPAGGQVHPAARPRTRPELRAGGRHRLWELQAPG 290
QY 94 RHSGPRRTQAQLRVGCVLGT-----CQVQNLHRLWQ-----LMGPAG 132
Db 291 AAVRPGRLARALPAGALGAGPVFARFAPGAPGCRGRRLSPRLLPQGAFFRPGLOG-AL 349
QY 133 RQDSA-----PVDPS 143
Db 350 RDDAERGAWPLDPTT 364

RESULT 4
US-09-252-991A-30689

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US-09-252-991A-24041
; Sequence 24041, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24041
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24041

Query Match      12.9%; Score 102.5; DB 4; Length 417;
Best Local Similarity 27.9%; Pred. No. 0.017;
Matches 36; Conservative 8; Mismatches 58; Indels 27; Gaps 3;

Qy 20 PGS-LRSLSGDRPVKPREPPARSPSSSQPRHPAPRPVVKLHRLAQRGAGLAFWM 78
Db 216 PGSGTHRALVGDHPHPPAGSRADAAPPQORAAAPHPVPCFARRRLSTGGGKPGRRFPFI 275
Qy 79 -----GQPLRDGGEQHSGRHSGPRRTQALLRVGCVLTGTCQVONLSHRLWQMGPA 132
Db 276 PRSAPPGHVSRGPPDPGDRPLHPR-----AHQQRERRAPPG 315
Qy 133 RQDSAPVDP 141
Db 316 PGRLLVPYR 324

RESULT 7
US-09-252-991A-30948
; Sequence 30948, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30948
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30948

Query Match      12.7%; Score 101; DB 4; Length 327;
Best Local Similarity 30.2%; Pred. No. 0.018;
Matches 54; Conservative 15; Mismatches 58; Indels 52; Gaps 11;

Qy 11 CISLLCLQLPGSLRSLSGGDRPVK-----PREPPARSPSS----- 46
Db 55 CLPLRLRTGTAGRQPGDGPAAKVAAGRGRPVAVLCARPLAPGRAPGAGDRRGR 114
Qy 47 ----SLQPRHPA----PRPVVKLHRA--LQARGAGLA--PVMGQPLRDGGRQHSQ--PR 93
Db 115 GRALSRQPRRAAGGQPEP-----HRAGLRARRRAGLACPATSRRLAAGRGVHGLHPA 169
Qy 94 RHSG-----PRRTQALLRVGCVLTGTCQVONLSHRLWQMGPAQDSAPVD---PSSP 144

US-09-252-991A-18286
; Sequence 18286, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18286
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18286

Query Match      12.7%; Score 100.5; DB 4; Length 528;
Best Local Similarity 28.0%; Pred. No. 0.036;
Matches 47; Conservative 9; Mismatches 43; Indels 69; Gaps 9;

Qy 28 GGDPRPVKP-----REPPARSPSSSQ---PRHPAPRPVVKLHRL 66
Db 52 GDDPVAADPRRGAWLPAGHPAGGADLRQPAALPGLALHLRVPRHPAVHPVAVLLHRL 111
Qy 67 QAO-----RGAGLAPVMQPIR--DGG-----RQHSGRPRISGPRPT 101
Db 112 QPECHTRPGLSQRLVPRRLQHLHGAGLRP---QHLRLHDGNLRRRDQEHAPRRSGGALRL 168
Qy 102 QAO-----LRVGCVLGTQCVONLS-----HRLWQMGPA 131
Db 169 HGRHLPLPAHRPALGAAPGTAVLQORSDDPDAFHLGGVHR--HSAGPA 214

RESULT 9
US-09-252-991A-25833
; Sequence 25833, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25833
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25833

Query Match      12.6%; Score 100; DB 4; Length 464;
Best Local Similarity 28.4%; Pred. No. 0.035;
Matches 42; Conservative 13; Mismatches 47; Indels 46; Gaps 9;

Qy 29 GDP-RPVK-----PREPPARSPSSSQPRHPA-----PRPVVKLHRLAQORGA 72
Db 185 GDHPRRGRRVPGPADAPAAAGRAGDQPRQGDHRHGAAAVAGHPAPAVLIRTHLSQRHRGP 244
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QY 73 GLAPVNGQPLR-----DGRQHSGRHSGRRRTQAQLLRVGCVLGTCOVNLS 121
Db 245 ARGP--RRPVQRAGDAPAPDGRH--RRNGLR--RRQLPR-----PVEGTD 290

QY 122 HRLW-----QLMGAPAGQDSAPVDPSSP 144
Db 291 RRAWPGRRHLEPEPGRRGHYPHPGP 318

RESULT 10
US-09-252-991A-18035
; Sequence 18035, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18035
; LENGTH: 783
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18035

Query Match 12.6%; Score 100; DB 4; Length 783;
Best Local Similarity 27.2%; Pred. No. 0.064;
Matches 44; Conservative 12; Mismatches 56; Indels 50; Gaps 7;

QY 19 LPGLSRLSGDPRPVKPREPPA---RSPSSSLQPRHPAPRPVVKLRLALQORGAGLA 75
Db 3 LPTARPRSGADRPQTEPARPPAAGRRVPAAGLGRGAVQPRP-----AGLR 48

QY 76 PVMGQPLRDGGRHSGRR---HSGPRTQAQLLRVG-----CVLGT--CQVQLSH 122
Db 49 PCI---LHPOGQADPLRAVPAERPARTGLARRAGKGAREDLAVRGTRILPVDRRYR 105

QY 123 RLWQLMGPA-----GRQDSAPVDPSSPHSY 147
Db 106 RAGRRRPAPLRGIEGKTRRRRPVRQRTQASARPSPHRY 147

RESULT 11
US-09-252-991A-30146
; Sequence 30146, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30146
; LENGTH: 763
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30146

Query Match 12.5%; Score 99.5; DB 4; Length 763;
Best Local Similarity 25.7%; Pred. No. 0.07;
Matches 55; Conservative 12; Mismatches 72; Indels 75; Gaps 8;

QY 3 RIFTAALGCTISLCLQLPQSLSRSLG-----GDRPV-----KPREPPARS 43
Db 10 RRPVAP-GLVAALPAAWPTARRRRTGRIHAAGARSAPVAPGGPRVAPRRHRRPGHPFAVA 68

QY 44 PSSSLQPRHPA-----PRPVVKLRLALQORGAGLAPVNGQPLRDGGRHSGRRHSGP 98
Db 69 PDRSLPAAGFAAARRRPRGAGGQRR--RARRGAGTAERRRRKPEDAAGRAGSAVORHGGL 126

QY 99 RR-----TQAQLL-----RVGCVLGTQOVNLS 121
Db 127 RQVPLPAGRAGRRLRORLARTLVLRQAALAFRRCHRRGVGQPGRLGTVRHAGLR 186

QY 122 HR-----LWQLMGAPAGQDSAPVDPSSP 144
Db 187 PRGAQGRVHPVDPVRQKRGGDRPRRCPADHARP 220

RESULT 12
US-09-252-991A-24961
; Sequence 24961, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24961
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24961

Query Match 12.5%; Score 99; DB 4; Length 373;
Best Local Similarity 31.4%; Pred. No. 0.034;
Matches 44; Conservative 10; Mismatches 46; Indels 40; Gaps 8;

QY 24 SRSLGSDPRPVKPREPPARSFSSSLQPRHPA---PRPVVKLRLALQORGAGLAPVNGQ 81
Db 93 ARLRGAVPREARP--PPGARRSGRTHRPLAEDARPL-----AGHADPGHGTAPHRAYP 144

QY 82 LRDGGRHSG-----GPRRH--SGPR-----TQAQLLRVGCVLGTQOVNLSHR 123
Db 145 ASPPGRRGQQLPPVARRGAFGPRRAAGHRDSFGDRRAPRLRRGVQLQPC-LQALE-- 201

QY 124 LWQLMGAPAGQDSAPVDPSS 143
Db 202 -----RHDAAPVSPAA 212

RESULT 13
US-09-252-991A-30690
; Sequence 30690, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

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; SEQ ID NO 30690
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30690

Query Match      12.5%; Score 99; DB 4; Length 588;
Best Local Similarity 28.9%; Pred. No. 0.058;
Matches 48; Conservative 10; Mismatches 45; Indels 62; Gaps 9;

QY 21 GSLSPSLGDP-RPVKP-----REPPSPSSSLQPRHP-----A 54
DB 266 GAGRELLGNPAAPRRGILLAHPOPAARGRRRPAARQFTALAPRRPLALVRHPRAGLQ 325
QY 55 PRPVVWKLHRAALQAQRGAGLAPVMQOPLRDGGRQHSPPR-----HSG-----PRR 100
DB 326 PRP-----QSRGAPDRGGQGHLLHRRGEQPAARERTPLPHAGKHQRDILLHRRR 376
QY 101 TQOALLRVGCVLTGCQVQNLHRLWQLMG-----PAGRODSAPVDP 141
DB 377 TQOQLRQ---PLGTARV-----RLQPGMGAAQRPPSDRHQPAPARP 414

RESULT 14
US-09-252-991A-30542
; Sequence 30542, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30542
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30542

Query Match      12.4%; Score 98.5; DB 4; Length 176;
Best Local Similarity 31.8%; Pred. No. 0.016; 50; Indels 45; Gaps 8;
Matches 47; Conservative 6; Mismatches 50; Indels 45; Gaps 8;

QY 31 PRPVKPREPPARSPSSSLQPRHPAP--RPVWKLHRAALQAQRGAGLA-----75
DB 40 PRPVL---PARQGPRESQQHPAPPLRPG---HARRAARILLAAAQRRRAAGGPAGR 91
QY 76 -----PVMGQPLRDGGRQHSGP---RRHSGPRRTQOQLRV-----GCVLTGCQV 117
DB 92 RLRSRPRRQOPLR---RQQLPAAARRGPGRTNRQALRQAGSRPQFGGATGRPQR 148
QY 118 QNLHRLWQLMGPAG-RQDSAPVDPSSP 144
DB 149 RRLCRRGRLEAAGRPALLPADPGRP 176

RESULT 15
US-09-252-991A-23976
; Sequence 23976, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

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; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23976
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23976

Query Match      12.4%; Score 98.5; DB 4; Length 275;
Best Local Similarity 26.9%; Pred. No. 0.027;
Matches 45; Conservative 16; Mismatches 53; Indels 53; Gaps 8;

QY 16 CLQLPGSLSLGSG--DPRPVKPRE--PPAESPSSSSLQPRHPAPRPVWKLHRAALQAQRG 71
DB 11 CORAAGAADRERRGQRLDPRQSRPRRHADSVDTFVQGGKPAQP-----VORDRG 58
QY 72 -----AGLAPVMGQPLRDGGRQHSGPRRHSGPRR-----TQOQL-LRV 108
DB 59 LRPPGPRGDAGIAARLGLVLRERRGARRHYRPRQRMARRGKMGVPVQRLDETQAEFLRLDS 118
QY 109 GCVLTGCQVQ-----NLHRLWQLMGPAGRQDSAPVDPSSP 144
DB 119 QQLAGSRGTQLRDPGRPPQRTTRRAVRLQHSAGPAG---AAPAHPEPTP 162

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(without alignments)

371.444 Million cell updates/sec

Title: US-10-723-368-2

Perfect score: 794

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	254	32.0	47	17	US-10-723-368-5
3	108.5	13.7	311	16	US-10-437-963-202661
4	106.5	13.4	386	15	US-10-425-114-56462
5	105	13.2	413	16	US-10-437-963-109275
6	103	13.0	556	15	US-10-425-114-64514
7	101.5	12.8	179	16	US-10-767-701-35404
8	101	12.7	242	15	US-10-450-436-28
9	99.5	12.5	203	16	US-10-767-701-34727
10	99.5	12.5	19662	15	US-10-084-846A-6
11	98.5	12.4	851	16	US-10-437-963-192117
12	98.5	12.4	19695	15	US-10-084-846A-3
13	98	12.3	2527	16	US-10-408-765A-2462

14	98	12.3	2715	16	US-10-408-765A-866	Sequence 866, App
15	97.5	12.3	1003	14	US-10-094-749-2528	Sequence 2528, App
16	97.5	12.3	1003	16	US-10-476-397-3	Sequence 3, Appli
17	97	12.2	166	16	US-10-437-963-127672	Sequence 127672,
18	97	12.2	180	16	US-10-437-963-129246	Sequence 129246,
19	96.5	12.2	165	16	US-10-437-963-167266	Sequence 167266,
20	96.5	12.2	239	15	US-10-425-114-64208	Sequence 64208, A
21	96	12.1	406	14	US-10-104-047-3010	Sequence 3010, App
22	95.5	12.0	176	16	US-10-437-963-154265	Sequence 154265,
23	95.5	12.0	377	15	US-10-425-114-70610	Sequence 70610, A
24	95.5	12.0	710	14	US-10-104-047-3402	Sequence 3402, App
25	95	12.0	109	16	US-10-767-701-39423	Sequence 39423, A
26	94	11.8	277	15	US-10-425-114-65831	Sequence 65831, A
27	94	11.8	300	16	US-10-408-765A-2788	Sequence 2788, App
28	94	11.8	476	15	US-10-425-114-59285	Sequence 59285, A
29	93.5	11.8	619	14	US-10-156-761-10652	Sequence 10652, A
30	93	11.7	180	15	US-10-108-260A-3850	Sequence 3850, App
31	93	11.7	210	15	US-10-425-114-48955	Sequence 48955, A
32	93	11.7	247	15	US-10-424-599-230446	Sequence 230446,
33	93	11.7	509	16	US-10-471-450-11	Sequence 11, Appli
34	93	11.6	539	15	US-10-425-114-39176	Sequence 39176, A
35	92.5	11.6	171	15	US-10-424-599-150599	Sequence 150599,
36	92.5	11.6	242	16	US-10-408-765A-2717	Sequence 2717, App
37	92.5	11.6	19652	15	US-10-084-846A-7	Sequence 7, Appli
38	92	11.6	138	16	US-10-437-963-111390	Sequence 111390,
39	92	11.6	240	15	US-10-425-114-68908	Sequence 68908, A
40	92	11.6	428	16	US-10-767-701-46277	Sequence 46277, A
41	92	11.6	544	14	US-10-017-161-670	Sequence 670, App
42	92	11.6	614	16	US-10-437-963-154795	Sequence 154795,
43	92	11.6	19725	15	US-10-084-846A-4	Sequence 4, Appli
44	91.5	11.5	466	16	US-10-437-963-167964	Sequence 167964,
45	91	11.5	144	15	US-10-425-114-54915	Sequence 54915, A

ALIGNMENTS

RESULT 1
US-10-723-368-2
; Sequence 2, Application US/107233368
; Publication No. US20040204353A1
; GENERAL INFORMATION:
; APPLICANT: Sheau Yu Teddy Hsu
; TITLE OF INVENTION: Intermedin and Its Uses
; FILE REFERENCE: STAN-284
; CURRENT APPLICATION NUMBER: US/10723.368
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,327
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (101)...(147)
; OTHER INFORMATION: Mature peptide
US-10-723-368-2

Query Match 100.0%; Score 794; DB 17; Length 148;
Best Local Similarity 100.0%; Pred. No. 3.9e-57;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARIPTAALGICSLICLQLPGSLRSRGDPRPVKPREPPARSPSSSLQPRHPAPRPVW 60
DB 1 MARIPTAALGICSLICLQLPGSLRSRGDPRPVKPREPPARSPSSSLQPRHPAPRPVW 60
QY 61 KLHRLAQRGAGLAPVMGQFLRDGGRQHSGRFRHSGRRTQAQLLRVGVLTGCVQNL 120

Db 61 KLHRLAQAGAGLAVMGQPLRDGGRHSGPRRHSGPRRTQAQLLRVGCVLTCQVNL 120
 QY 121 SHRLWLMGPAGQDSAPVDPSSPHSYG 148
 Db 121 SHRLWLMGPAGQDSAPVDPSSPHSYG 148

RESULT 2

US-10-723-368-5
 ; Sequence 5, Application US/10723368
 ; Publication No. US20040204353A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheau Yu Teddy Hsu
 ; TITLE OF INVENTION: Intermedin and Its Uses
 ; FILE REFERENCE: STAN-284
 ; CURRENT APPLICATION NUMBER: US/10/723,368
 ; CURRENT FILING DATE: 2003-11-26
 ; PRIOR APPLICATION NUMBER: 60/429,327
 ; PRIOR FILING DATE: 2002-11-26
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 47
 ; TYPE: PRT
 ; ORGANISM: H. sapiens
 ; US-10-723-368-5

Query Match 32.0%; Score 254; DB 17; Length 47;
 Best Local Similarity 100.0%; Pred. No. 1.1e-13;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 TQQLLRVGCVLTCQVNLSHRLWLMGPAGQDSAPVDPSSPHSY 147
 Db 1 TQQLLRVGCVLTCQVNLSHRLWLMGPAGQDSAPVDPSSPHSY 47

RESULT 3

US-10-437-963-202661
 ; Sequence 202661, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 202661
 ; LENGTH: 311
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(311)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_9791C.1.pep
 ; US-10-437-963-202661

Query Match 13.7%; Score 108.5; DB 16; Length 311;
 Best Local Similarity 27.7%; Pred. No. 0.5;
 Matches 44; Conservative 13; Mismatches 67; Indels 35; Gaps 8;

QY 20 PGSLSRLGGDRPV-----KPPEPP--ARSPSSSLQPRHPAPR---PVMVKLHR 64

Db 48 PAGLSPSPSPAPASPPSPASPHRHPRPPEPRRVRPRRPRRPRRPRRPLPLPFP 107
 QY 65 ALQAQAGAGLA-----PVMGQPLRDGGRHSGPRRHSG-----PRRT-QAQLLRV 108
 Db 108 SLPSYXGEPTAASFPFSLPSRPPLR---RAYGRRRRXPAGAAASRRPRXGRRARRV 164
 QY 109 GCVLGTQVQNLSHRLWLMGPAGQDSAPVDPSSPHSY 147
 Db 165 AAAWGPA-VSRPRVWLTRGAGAGRXPAGDPDPWTH 202

RESULT 4

US-10-425-114-56462
 ; Sequence 56462, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 56462
 ; LENGTH: 386
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: UC-ZMFLB73224A12_FLI.pep
 ; US-10-425-114-56462

Query Match 13.4%; Score 106.5; DB 15; Length 386;
 Best Local Similarity 28.1%; Pred. No. 0.91;
 Matches 45; Conservative 13; Mismatches 41; Indels 61; Gaps 9;

QY 1 MARIPTAALGCTISLLCQLQFSGLSRSLGDPVPRKPEPEARS-PSSSLQPRHPAP--- 55
 Db 98 LPRLPVLRRG-----LPRGGRAAAPRP-PAPRRPRRRLPLALQPRHRSPLPA 148
 QY 56 --RPVVVKL-----HR-----ALQAQAGAGLAPVMGQPL-----RDGGR 87
 Db 149 RRRRRWLLLSRRRHQQLEAVLRREGGVGPPAPGHEVGLPHGLRLRAAGAGPDGGR 208
 QY 88 QHSG---PRRHSG-----PRRTQAQLLRV 108
 Db 209 RRSGGARPRRAAGVQGRGRIHARAPRRRPRRGRRLRL 248

RESULT 5

US-10-437-963-109275
 ; Sequence 109275, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966

QY 124 LWQMGFAGQDSAPVDPSPSHSYG 148
 Db 129 -----GSGGR--SHPGGPGSPRG 146

RESULT 9
 US-10-767-701-34727
 ; Sequence 34727, Application US/10767701
 ; Publication No. US20040172684A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
 ; FILE REFERENCE: 38-21(53535)B
 ; CURRENT APPLICATION NUMBER: US/10/767,701
 ; CURRENT FILING DATE: 2004-01-29
 ; NUMBER OF SEQ ID NOS: 63128
 ; SEQ ID NO 34727
 ; LENGTH: 203
 ; TYPE: PRT
 ; ORGANISM: Sorghum bicolor
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C53158_1.pep
 US-10-767-701-34727

Query Match 12.5%; Score 99.5; DB 16; Length 203;
 Best Local Similarity 30.4%; Pred. No. 1.8;
 Matches 41; Conservative 10; Mismatches 43; Indels 41; Gaps 8;
 QY 17 LQLP---PGSLRSLSGDDP-RPVKPREPPARSPSSLSQPRHPAPRPVVKLHRAALQA---Q 69
 Db 12 LQLSPQGRQPSRAGAPRVRHRPGG-----PPRPPPRPPGAPDCHGGCID 64
 QY 70 RGAGLAPVMGQ-----LRDGGROHSPPRHSGPR-----TQALLRVG 109
 Db 65 GGAGAAPPFRPRPRAGRAPALPLRDG-----GPDGGGPRQPLLRKRTWNTTTSQAIVG 119
 QY 110 CVLGTQVQNLSHRL 124
 Db 120 A--NVCPISLDYEV 132

RESULT 10
 US-10-084-846A-6
 ; Sequence 6, Application US/10084846A
 ; Publication No. US2004006026A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEITNAUER, GABRIELE
 ; APPLICANT: MUHLENWEG, AGNES
 ; APPLICANT: TREFFZER, AXEL
 ; APPLICANT: BECHTHOLD, ANDREAS
 ; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
 ; FILE REFERENCE: 1974-005
 ; CURRENT APPLICATION NUMBER: US/10/084,846A
 ; CURRENT FILING DATE: 2003-02-25
 ; PRIOR APPLICATION NUMBER: PCT/EP01/09815
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: DE 101 09 166.4
 ; PRIOR FILING DATE: 2001-02-25
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: Patent In Ver. 3.2
 ; SEQ ID NO 6
 ; LENGTH: 19662
 ; TYPE: PRT
 ; ORGANISM: Streptomyces viridochromogenes
 ; FEATURE:
 ; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 2.
 ; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
 US-10-084-846A-6

Query Match 12.5%; Score 99.5; DB 15; Length 19662;

Best Local Similarity 28.9%; Pred. No. 1.7e+02;
 Matches 41; Conservative 11; Mismatches 49; Indels 41; Gaps 7;
 QY 17 LQLP-----GSLRSLSGDDPRPVKPREPPAR-SPSSLSQPRHPAPRPVVKLHRAALQA 68
 Db 4413 MRLPSTVVKFPEGLSRA--GQPRARPRSATGRFPAAPLRPSGPPRRRAVRSH----- 4465
 QY 69 QRGAGLAPVMGQPLRDGGRQHSQPRRHSGPRRTQALLRVGCVLGTQVQNLSHRLWQLM 128
 Db 4466 ----ACAPARCPA--GGRSSARRPRAPCAAGARPRSG-----R 4501
 QY 129 GPAGRODSAPVD--PSSPHSYG 148
 Db 4502 APAVPGGSAPESRRPARPPSHG 4523

RESULT 11
 US-10-437-963-192117
 ; Sequence 192117, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 192117
 ; LENGTH: 851
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_88372C.1.pep
 US-10-437-963-192117

Query Match 12.4%; Score 98.5; DB 16; Length 851;
 Best Local Similarity 26.4%; Pred. No. 9;
 Matches 43; Conservative 16; Mismatches 53; Indels 51; Gaps 8;
 QY 22 SLRSLSGDDPRPVKPREPP-----ARSPSSLSQ----- 50
 Db 3 SLQQGGGDPQPQQAAPALLGGADWLGFGRAAELDESVAASPASFLPPAPPVDARA 62
 QY 51 -RHPAPRPVVKLHRAALQAQRGAGLAPVMGQPLRDG---GROHSGPRRHSGPRRTQOAL 105
 Db 63 QAOPEKP---KOLGAVDVERHLALA---HONVRSKYEALHGNIVIEKNPRTD-NL 115
 QY 106 LRVGCVLGTQVQNLSHRLWQLMGPAGRODSAPVDPSPSHSYG 148
 Db 116 LLLGAIY--YQIRNYD-----MCIKNEEALAIENFAECYG 150

RESULT 12
 US-10-084-846A-3
 ; Sequence 3, Application US/10084846A
 ; Publication No. US2004006026A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEITNAUER, GABRIELE
 ; APPLICANT: MUHLENWEG, AGNES
 ; APPLICANT: TREFFZER, AXEL
 ; APPLICANT: BECHTHOLD, ANDREAS
 ; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
 ; FILE REFERENCE: 1974-005
 ; CURRENT APPLICATION NUMBER: US/10/084,846A
 ; CURRENT FILING DATE: 2003-02-25

; PRIOR APPLICATION NUMBER: PCT/EP01/09815
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: DE 101 09 166.4
 ; PRIOR FILING DATE: 2001-02-25
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 3
 ; LENGTH: 19695
 ; TYPE: PRT
 ; ORGANISM: Streptomyces viridochromogenes
 ; FEATURE:
 ; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 1.
 ; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
 US-10-084-846A-3

Query Match 12.4%; Score 98.5; DB 15; Length 19695;
 Best Local Similarity 27.8%; Pred. No. 2.1e+02;
 Matches 40; Conservative 7; Mismatches 34; Indels 63; Gaps 7;
 Qy 29 GDRPVK---PREPPARSPSS---LQPHPA--PRPVVK-----61
 Db 6166 GDRPVK---PREPPARSPSS---LQPHPA--PRPVVK-----61
 Qy 62 -----LHRAIQORAGL-----APVMOPLRDG-----GRHSGP---92
 Db 6226 PCGPRTGAHRAHPRPRAGAGRNPFVGRGLPGGAPPGRARRAGRGGRGLGRAHPGPSAV 6285
 Qy 93 -----RRHSGPRRTQAQLRVG 109
 Db 6286 PAGPPGRRGRDRPGRTGRRARAG 6309

RESULT 13
 US-10-408-765A-2462
 ; Sequence 2462, Application US/10408765A
 ; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Faby, Eoin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.
 ; APPLICANT: Glenn, Gary M.
 ; APPLICANT: Warnock, Dale E.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; FILE REFERENCE: 660088.465
 ; CURRENT APPLICATION NUMBER: US/10/408,765A
 ; CURRENT FILING DATE: 2003-04-04
 ; NUMBER OF SEQ ID NOS: 3077
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2462
 ; LENGTH: 2527
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-765A-2462

Query Match 12.3%; Score 98; DB 16; Length 2527;
 Best Local Similarity 31.9%; Pred. No. 29;
 Matches 37; Conservative 10; Mismatches 51; Indels 18; Gaps 5;
 Qy 29 GDRPVKPREPPARSPSSLOPRHPAPRPVVMKHLRAIQORAGLAPVMOPLRDGGRQ 88
 Db 484 GAPEAPEPEPPADD-----SPAEPPEPRVAGRTNLSLPR-----FAPVVTTPVKAAYSP 533
 Qy 89 HSGPRRHSGPRRTQAQLRVGCVLTGTCQVQNLSHRL-----WOLMGPAQRQDSAPVD 140
 Db 534 HGAPALSNGP-QTQAQLIQ---PLQALQTQLLPQALPPPPQLOPPSPQMPPLLE 585

RESULT 14
 US-10-408-765A-866
 ; Sequence 866, Application US/10408765A

; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Faby, Eoin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.
 ; APPLICANT: Glenn, Gary M.
 ; APPLICANT: Warnock, Dale E.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
 ; FILE REFERENCE: 660088.465
 ; CURRENT APPLICATION NUMBER: US/10/408,765A
 ; CURRENT FILING DATE: 2003-04-04
 ; NUMBER OF SEQ ID NOS: 3077
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 866
 ; LENGTH: 2715
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-765A-866

Query Match 12.3%; Score 98; DB 16; Length 2715;
 Best Local Similarity 31.9%; Pred. No. 31;
 Matches 37; Conservative 10; Mismatches 51; Indels 18; Gaps 5;
 Qy 29 GDRPVKPREPPARSPSSLOPRHPAPRPVVMKHLRAIQORAGLAPVMOPLRDGGRQ 88
 Db 672 GAPEAPEPEPPADD-----SPAEPPEPRVAGRTNLSLPR-----FAPVVTTPVKAAYSP 721
 Qy 89 HSGPRRHSGPRRTQAQLRVGCVLTGTCQVQNLSHRL-----WOLMGPAQRQDSAPVD 140
 Db 722 HGAPALSNGP-QTQAQLIQ---PLQALQTQLLPQALPPPPQLOPPSPQMPPLLE 773

RESULT 15
 US-10-094-749-2528
 ; Sequence 2528, Application US/10094749
 ; Publication No. US20030219741A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: WAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUUKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUKA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: IRIE, RYOTARO
 ; APPLICANT: TAMECHIKA, ICHIRO
 ; APPLICANT: SEKI, NAHICO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTOTYUKI
 ; APPLICANT: NAGAHARI, KENJI
 ; APPLICANT: MASUHO, YASUHIKO
 ; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
 ; FILE REFERENCE: 084335/0160
 ; CURRENT APPLICATION NUMBER: US/10/094,749
 ; CURRENT FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: 60/350,435
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: JP 2001-328381
 ; PRIOR FILING DATE: 2001-09-14
 ; NUMBER OF SEQ ID NOS: 3381
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2528
 ; LENGTH: 1003
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-094-749-2528

Search completed: October 22, 2004, 09:06:05
Job time : 130 secs

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OM protein - protein search, using sw model

Run on: October 22, 2004, 08:37:31 ; Search time 154 Seconds

(without alignments)
344.753 Million cell updates/sec

Title: US-10-723-368-2

Perfect score: 794

Sequence: 1 MARIPTAALGICSLCLQLP.....GPAGRQDSAPVDPSPSPHSYG 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04.*

1: Genesep1980s.*

2: Genesep1990s.*

3: Genesep2000s.*

4: Genesep2001s.*

5: Genesep2002s.*

6: Genesep2003as.*

7: Genesep2003bs.*

8: Genesep2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	794	100.0	148	8	ADO61520 Human int
2	254	32.0	47	8	ADO61523 Human int
3	110	13.9	379	7	ABO78178 Pseudomon
4	108	13.6	362	7	ABO82895 Pseudomon
5	107.5	13.5	514	7	ABO79462 Pseudomon
6	103.5	13.0	621	7	ABO81943 Pseudomon
7	103.5	13.0	1938	6	ABE98398 Streptomy
8	103	13.0	142	7	ABO72835 Pseudomon
9	102.5	12.9	417	7	ABO75295 Pseudomon
10	101	12.7	242	3	AY96318 Mammalian
11	101	12.7	242	5	ABG32397 Human JFY
12	101	12.7	327	7	ABO82202 Pseudomon
13	100.5	12.7	528	7	ABO69540 Pseudomon
14	100	12.6	464	7	ABO77087 Pseudomon
15	100	12.6	555	4	ABG16571 Novel hum
16	100	12.6	783	7	ABO69289 Pseudomon
17	99.5	12.5	763	7	ABO81400 Pseudomon
18	99	12.5	373	7	ABO76215 Pseudomon
19	99	12.5	588	7	ABO81944 Pseudomon
20	98.5	12.4	176	7	ABO81796 Pseudomon
21	98.5	12.4	275	7	ABO75230 Pseudomon
22	98.5	12.4	307	4	ABG04221 Novel hum
23	98.5	12.4	362	7	ABO82270 Pseudomon
24	98.5	12.4	364	7	ABO71177 Pseudomon
25	98.5	12.4	498	7	ABO73227 Pseudomon

ALIGNMENTS

RESULT 1

ADO61520

ID ADO61520 standard; protein; 148 AA.

XX ADO61520;

XX 26-AUG-2004 (first entry)

XX Human intermediate SEQ ID NO:2.

XX human; intermediate; hypotensive; gene therapy; hypertension;
cardioprotective; diet; prolactin release; growth hormone release;
ovarian follicle survival; oedema.

OS Homo sapiens.

XX WO2004048547-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US037968.

XX 26-NOV-2002; 2002US-0429327P.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Hsu SYT;

XX WPI; 2004-441176/41.

XX N-ESDB; ADO61519.

New composition comprises an intermediate peptide, useful for treating hypertension, as cardioprotective agent, as a diet aid, for the release of prolactin, or for growth hormone release from the pituitary.

Claim 1; SEQ ID NO 2; 68pp; English.

The invention relates to a novel composition comprising an intermediate peptide, which comprises at least 18 contiguous amino acids in a sequence comprising 148 amino acids (ADO61520). A composition of the invention has cardioprotective activity, and may have a use in gene therapy. The composition comprising the intermediate peptide is useful for identifying homologous or related genes, for production of the encoded peptide, in producing compositions that modulate the expression or function of its encoded protein, for gene therapy, mapping functional regions of the protein, or in studying associated physiological pathways. The intermediate peptide is useful for treating hypertension, as a cardioprotective agent, as a diet aid, for the release of prolactin, in growth hormone release from the

ABO83358 Pseudomon
ABO76021 Pseudomon
ABO81792 Pseudomon
ADJ70656 Human hea
ADJ69060 Human hea
ABO67968 Pseudomon
ABO75829 Pseudomon
ABO82371 Pseudomon
ADA54960 Human pro
ABP58226 Human cel
ABO82380 Pseudomon
ABO72672 Pseudomon
ABO83169 Pseudomon
ABG14738 Novel hum
ABO80092 Pseudomon
ABO82545 Pseudomon
ABO72876 Pseudomon
AAB49765 Human pro
AAB88393 Human mem
ABO83239 Pseudomon

26 98.5 12.4 642 7 ABO83358
27 98.5 12.4 642 7 ABO76021
28 98 12.3 266 7 ABO81792
29 98 12.3 2527 7 ADJ70656
30 98 12.3 2715 7 ADJ69060
31 97.5 12.3 142 7 ABO67968
32 97.5 12.3 416 7 ABO75829
33 97.5 12.3 436 7 ABO82371
34 97.5 12.3 1003 6 ADA54960
35 97.5 12.3 1003 6 ABP58226
36 97 12.2 317 7 ABO82380
37 97 12.2 653 7 ABO72672
38 97 12.2 720 7 ABO83169
39 97 12.2 781 4 ABG14738
40 96.5 12.2 230 7 ABO80092
41 96.5 12.2 392 7 ABO82545
42 96.5 12.2 538 7 ABO72876
43 96.5 12.2 571 4 AAB49765
44 96.5 12.2 571 4 AAB88393
45 96 12.1 260 7 ABO83239

Db 70 LPHVGLRRPLIAVVGHRPADRHVRHLQLQCTAVRILQHGFAFPDRAVTRVQHGAARPA 129
 QY 46 SSL-----QPRHPAPRPVVKLHRAALQAGAGLAPVMGQPLRDGGRHSGPRRHSG 97
 Db 130 RELVRLGREGPRPALRLLSAEYHRP-PATTHGIG-----RQERAGRHAG 177
 QY 98 PRTQAQLRLVGCVLGTQVQNLHRLWLMGPAQRDSAPVDPSSPHSYG 148
 Db 178 HQHREAG-----DLGWCRQLORPA-RLPSVAAP-----RHPVDPGGLHRPG 216

RESULT 4
 ABO82895
 ID ABO82895 standard; protein; 362 AA.
 AC ABO82895;
 DT 29-JUL-2004 (first entry)
 DE Pseudomonas aeruginosa polypeptide #15070.
 DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 KW Pseudomonas aeruginosa.
 OS US6551795-B1.
 FN 22-APR-2003.
 PD 18-FEB-1999; 99US-00252991.
 PF 18-FEB-1998; 98US-0074788P.
 PR 27-JUL-1998; 98US-0094190P.
 PR (GENO-) GENOME THERAPEUTICS CORP.
 PA Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 PI WPI; 2003-615309/58.
 DR N-PSDB; ABD16466.
 DR Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX Disclosure; SEQ ID NO 31641; 455pp; English.
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABO67826-
 CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX Sequence 362 AA;
 SQ

Query Match 13.6%; Score 108; DB 7; Length 362;
 Best Local Similarity 32.9%; Pred. No. 0.083;
 Matches 50; Conservative 16; Mismatches 42; Indels 44; Gaps 10;
 QY 17 LQLPGSLRSR--LGGDRPVKPK-----REP---PARSPSS- 47
 Db 206 LRLRNLARTRCAGGLPRPAPGGRQWAPRGRGAPGQPADWRRAFCGFGRTVVAAR 265

QY 48 --LOPHRAPRPVVKLHRAALQAGAGLAPVMGQPLRDGGRHSGPRRHSGPRRTOAOL 105
 Db 266 RDLREYGAAPRAIRRRR--RADHGATAA---GGVAGEGQPPASGPRQ---PRRARAR 317
 QY 106 LRVGCVLTQCVQNLHRLWLMGPAQRDS 137
 Db 318 RQAGOV-GKDGQPOQSR--LPGF-GRAPGA 344
 RESULT 5
 ABO79462
 ID ABO79462 standard; protein; 514 AA.
 AC ABO79462;
 DT 29-JUL-2004 (first entry)
 DE Pseudomonas aeruginosa polypeptide #11637.
 DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 KW Pseudomonas aeruginosa.
 OS US6551795-B1.
 FN 22-APR-2003.
 PD 18-FEB-1999; 99US-00252991.
 PF 18-FEB-1998; 98US-0074788P.
 PR 27-JUL-1998; 98US-0094190P.
 PR (GENO-) GENOME THERAPEUTICS CORP.
 PA Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 PI WPI; 2003-615309/58.
 DR N-PSDB; ABD13033.
 DR Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX Disclosure; SEQ ID NO 28208; 455pp; English.
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABO67825-
 CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX Sequence 514 AA;
 SQ

Query Match 13.5%; Score 107.5; DB 7; Length 514;
 Best Local Similarity 27.7%; Pred. No. 0.13;
 Matches 54; Conservative 11; Mismatches 51; Indels 79; Gaps 11;
 QY 20 PGSLSRSI-----GGDPR---PVKPREPPARS-----PSSSLQP-- 50
 Db 178 PGRFRALPARLQTAEDRRGKPGAPAGADPRAYFPFQPPWRGCRALFGSLRPAG 237

QY 51 -RHPAPRPVVKLHRLAQORAGLAPVMGQ-----PLRDGGQHOH-----SGPR 93
Db 238 EHEQRP-----CRRAPCQPGVLPAGQAVHPAARPRTRPELRAGGRHWRLQAPG 290
QY 94 RHSGPRTQQLRVGCVLGT-----CQVQLSHRLWQ-----LMGPAG 132
Db 291 AAVRPGQLARALPAGAALGAGPVFAFPAGPGACRGRLSPRLLOPQAFRPGLOQ-AL 349
QY 133 RODSA-----PVDPS 143
Db 350 RDDAERGAWPLDPTT 364

RESULT 6
ABO81943
ID ABO81943 standard; protein; 621 AA.
AC ABO81943;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #14118.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR N-PSDB; ABD15514.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 30689; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
XX polynucleotides encoding them. The sequences are useful in diagnosis and
XX therapy of pathological conditions, as molecular targets for diagnostics,
XX prophylaxis and treatment of pathological conditions resulting from a
XX bacterial infection, for evaluating a compound, such as a polypeptide,
XX for the ability to bind a P. aeruginosa nucleic acid, as components of
XX effective antibacterial targets, as targets for antibacterial drugs,
XX including anti-P. aeruginosa drugs, as templates for recombinant
XX production of P. aeruginosa-derived peptides or polypeptides, as target
XX components for diagnosis and/or treatment of P. aeruginosa-caused
XX infection, and in detection of P. aeruginosa sequences or other sequences
XX of Pseudomonas species using biochip technology. Sequences ABO81943-
XX ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
XX sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html
XX
SQ Sequence 621 AA;
Query Match 13.0%; Score 103.5; DB 7; Length 621;
Best Local Similarity 28.4%; Pred. No. 0.39;
Matches 40; Conservative 13; Mismatches 45; Indels 43; Gaps 7;

QY 31 PRPVKPREPPARSSSSLOPQHPAPRPVVKLHRLAQORAGLAPVMGQPLRDGGR--- 87

Db 421 PDPARTQPP-ROMLLAVAPGQRPREV-----ESRPAHQPALAP--GPPIRRAGALAY 472
QY 88 --OHSGRPRHSGPRRTQAQLLRVGCVLGTQVQNL--SHRLWQL-----127
Db 473 PSEHGARRHADPR-----GTAAQORLAASRALRQHAGAARPAAGNRRRAGD 520
QY 128 MGPAQRQDSAPVDPSPSHSYG 148
Db 521 LPDAGRRHRVHAAAPAPRATG 541

RESULT 7
ABB98398
ID ABB98398 standard; protein; 19938 AA.
AC ABB98398;
XX
DT 05-MAR-2003 (first entry)
XX
DE Streptomyces viridochromogenes Avi gene cluster polypeptide frame 1.
XX
KW Avilamycin; antibacterial; virucide; protozoacide; fungicide; infection;
XX medicine; Staphylococcus aureus; biosynthetic gene cluster; enzyme.
XX
OS Streptomyces viridochromogenes.
XX
PN WO200268436-A1.
XX
PD 06-SEP-2002.
XX
PF 24-AUG-2001; 2001WO-EP009815.
XX
PR 25-FEB-2001; 2001DE-01009166.
XX
PA (COMB-) COMBINATURE BIOPHARM AG.
XX
PI Weitnauer G, Muehlenweg A, Trefzer A, Bechthold A;
XX
DR WPI; 2003-018650/01.
DR N-PSDB; ABZ37515.
XX
PT New avilamycin derivatives, useful for treatment of infections, and
XX nucleic acid encoding avilamycin synthesis enzymes.
XX
PS Example 1; Page 68-301; 319pp; German.
XX
CC The invention relates to avilamycin derivatives (I) with antibacterial,
XX virucide, protozoacide and fungicide activity. (I) are useful for
XX treatment of infections (bacterial, viral, protozoal or fungal), in human
XX or veterinary medicine, particularly where caused by Staphylococcus
XX aureus. (I) are more hydrophilic than known avilamycins. The present
XX sequence is that of an avilamycin synthesis enzyme from the Streptomyces
XX viridochromogenes Avilamycin A biosynthetic gene cluster (ABZ37515-
XX ABZ37516)
XX
SQ Sequence 19938 AA;
Query Match 13.0%; Score 103.5; DB 6; Length 19938;
Best Local Similarity 35.3%; Pred. No. 16;
Matches 36; Conservative 7; Mismatches 38; Indels 21; Gaps 5;

QY 18 QLPGSLRSRSGGPRPVKPREPPARSSSSLOPQHPA---PRPVVKLHR---ALQORQ 71
Db 8501 EPTSTVTR---GPPRRPRRPAFPQRRRALAGFAVADARFAGGLHRCRGAARAGHG 8557

QY 72 AGI-----APVMGQPLRDGGQFQHSQPRRH--SGPRRT 101
Db 8558 RGLHRRGLPQGRPAPLVTLPGRGERTHXPXPRRHWTGPRRS 8599

RESULT 8
ABO72835

ID AB072835 standard; protein; 142 AA.
 AC AB072835;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Pseudomonas aeruginosa polypeptide #5010.
 XX
 KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 XX
 OS Pseudomonas aeruginosa.
 XX
 GN
 XX
 FN US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 XX
 PR 27-JUL-1998; 98US-0094190P.
 XX
 XX (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX
 DR WPI; 2003-615309/58.
 DR N-PSDB; ABD06406.
 XX
 PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 21581; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences AB067826-
 CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 142 AA;
 Query Match 13.0%; Score 103; DB 7; Length 142;
 Best Local Similarity 39.3%; Pred. No. 0.09;
 Matches 35; Conservative 6; Mismatches 34; Indels 14; Gaps 7;
 QY 25 RSLGDP---RPVKPRPPARSPSSLSQPRH--PAP-PPVVKLHRLAQQR-CAGLAP 76
 DB 11 RTRGGPAAQRALQPRPP---PGACQQRRLLPAPERPRPWARRRRRTAGVAVIP 67
 QY 77 VMGQPLRDGGRQHS--PRRHSGRRTQA 103
 DB 68 -RTQEPQGTGPRGPRHPRRAPRA 95
 RESULT 9
 ABO75295
 ID ABO75295 standard; protein; 417 AA.
 XX
 AC ABO75295;
 XX
 DT 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #7470.
 DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 KW
 XX
 OS Pseudomonas aeruginosa.
 XX
 FN US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 XX
 PR 27-JUL-1998; 98US-0094190P.
 XX
 XX (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX
 DR WPI; 2003-615309/58.
 DR N-PSDB; ABD08866.
 XX
 PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 24041; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences AB067826-
 CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 417 AA;
 Query Match 12.9%; Score 102.5; DB 7; Length 417;
 Best Local Similarity 27.9%; Pred. No. 0.32;
 Matches 36; Conservative 8; Mismatches 58; Indels 27; Gaps 3;
 QY 20 PGS-LRSRLGDPREPVKPREPPARSPSSLSQPRHPPVPVVKLHRLAQQRGAGLAPV 78
 DB 216 PGSGTHRALVGDHPHPAGSRADAAPPQORAAHPVPCFARRRLSTGGGGKPGRRFFGI 275
 QY 79 -----GQPLRDGGRQHSGRPRRRTQAQLLRVGCVLGTCQVQNLHRLWLQMGFAG 132
 DB 276 PRSAPPGHFVSGRPPDPGDFRPLHPR-----AHQORRRRAPP 315
 QY 133 QDSAPVDP 141
 DB 316 PGRLLFVRP 324
 RESULT 10
 AAY96318
 ID AAY96318 standard; protein; 242 AA.
 XX
 AC AAY96318;
 XX
 DT 17-AUG-2000 (first entry)

DE Mammalian putative apoptosis regulator BBC3-ORF1.
 XX Mammal; apoptosis; cell death; BBC3; apoptosis promotion;
 KW apoptosis inhibition; malignant cell; autoimmune disease.
 XX Mammalia.

XX WO2000026228-A1.
 XX 11-MAY-2000.

XX 28-OCT-1999; 99WO-US025285.
 XX 02-NOV-1998; 98US-00184168.

XX (CLON-) CLONTECH LAB INC.

XX Zhu L, Yin X, Chittenden T;
 XX WPI; 2000-365560/31.
 DR N-PSDB; AAA30239.

XX Novel polynucleotide encoding a BBC3 protein which is useful for
 PT modulating apoptosis, especially in the treatment of cancer and
 PT autoimmune diseases.

XX Example 3; Page 41-42; 47pp; English.

XX The present sequence is a putative version of the mammalian apoptosis
 CC regulator BBC3, and has been designated BBC3-ORF1. the protein, nucleic
 CC acids and antibodies are suitable for use in promoting cell death or for
 CC preventing apoptosis in malignant cells and those causing autoimmune
 CC diseases

XX Sequence 242 AA;

Query Match 12.7%; Score 101; DB 3; Length 242;
 Best Local Similarity 29.7%; Pred. No. 0.25;
 Matches 43; Conservative 9; Mismatches 57; Indels 36; Gaps 7;

QY 18 QLPGLSLRSLGGDPKVPKPREPPSPSS-----SLOPR--HPAPRPVWKLH 63
 Db 24 QLPGAR-----GPGPRRPAPLPARPPGALGSLRPLRARPGRPRRPHPAARCLPLRPH 78

QY 64 RALQAGAGLAPVMGQPLDGGHSGRRHSGPRRTQALLRVGCVLTCQVONLSHR 123
 Db 79 RPTRRHRRPG-----GFPLAWGSPQ---PAPRPAPGRSSALALAGGAAPGVARAQRPG-- 128

QY 124 LWQLMGPAGQDSAPVDPSPSPHSYG 148
 Db 129 -----GSGGR--SHPGGPGSPRGGG 146

RESULT 11
 ABG32397
 ID ABG32397 standard; protein; 242 AA.

XX AC ABG32397;
 XX DT 15-NOV-2002 (first entry)

XX Human JFY1 associated protein.

XX Human; JFY1; apoptosis; cancer; cellular proliferation; p53;
 KW gene therapy; neoplastic cancer cell.

XX Homo sapiens.
 XX WO200264790-A2.

XX 22-AUG-2002.

XX 12-DEC-2001; 2001WO-US047455.

XX 19-DEC-2000; 2000US-0256328P.
 XX (UYJO) UNIV JOHNS HOPKINS.

XX Yu J, Kinzler KW, Vogelstein B;
 XX WPI; 2002-643485/69.

XX New JFY1 proteins and nucleic acids, useful for inducing rapid apoptosis
 PT in cancer cells, for treating cancers or other diseases characterized by
 PT unwanted cellular proliferation, and as a substitute for p53 in cancer
 PT gene therapy.

XX Disclosure; Page 43-44; 45pp; English.

XX The invention relates to an isolated and purified JFY1 coding sequence
 CC and purified JFY1 protein. The JFY1 polynucleotide is useful for inducing
 CC rapid apoptosis in cancer cells, for treating cancers or other diseases
 CC characterised by unwanted cellular proliferation, and as a substitute for
 CC p53 in cancer gene therapy. The expression product of JFY1 may be used as
 CC an indicator for neoplastic cancer cells and in determining the prognosis
 CC of a cancer patient. The present sequence represents the amino acid
 CC sequence of a human JFY1 associated protein

XX Sequence 242 AA;

Query Match 12.7%; Score 101; DB 5; Length 242;
 Best Local Similarity 29.7%; Pred. No. 0.25;
 Matches 43; Conservative 9; Mismatches 57; Indels 36; Gaps 7;

QY 18 QLPGLSLRSLGGDPKVPKPREPPSPSS-----SLOPR--HPAPRPVWKLH 63
 Db 24 QLPGAR-----GPGPRRPAPLPARPPGALGSLRPLRARPGRPRRPHPAARCLPLRPH 78

QY 64 RALQAGAGLAPVMGQPLDGGHSGRRHSGPRRTQALLRVGCVLTCQVONLSHR 123
 Db 79 RPTRRHRRPG-----GFPLAWGSPQ---PAPRPAPGRSSALALAGGAAPGVARAQRPG-- 128

QY 124 LWQLMGPAGQDSAPVDPSPSPHSYG 148
 Db 129 -----GSGGR--SHPGGPGSPRGGG 146

RESULT 12
 AB082202
 ID AB082202 standard; protein; 327 AA.

XX AC AB082202;

XX DT 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #14377.

XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 XX Pseudomonas aeruginosa.

XX US6551795-B1.

XX 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

XX 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

XX N-PSDB; ABD15773.

PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 25833; 455pp; English.
 XX

CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences AB067826-
 CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 464 AA;

Query Match 12.6%; Score 100; DB 7; Length 464;
 Best Local Similarity 28.4%; Pred. No. 0.61;
 Matches 42; Conservative 13; Mismatches 47; Indels 46; Gaps 9;
 QY 29 GDP-RPVK-----PREPARSPSSLOPRHPA-----PPVVKLHRLAQAQGA 72
 DB 185 GDHPRGRRVPGPADAPAAAGRGDQPRQPDGRHGAAGAAVAGHPAPAVIRHLSGRHRGP 244
 QY 73 GLAPVVMGQPLR-----DGRHSGPRHSGPRRTQAQLLRVGCVLGTCCVQNL 121
 DB 245 ARGP--RRPVQRAGDAPAPADPGRRH---RRGNGLRR--RQLPR-----PVEGTD 290
 QY 122 HRLW-----QLMGPAQDSAPVDPSPP 144
 DB 291 RRAWPGRRHLEPPEPGRGRGHFAVHPGPP 318

RESULT 15
 ABG16571
 ID ABG16571 standard; protein; 555 AA.
 XX
 AC ABG16571;

XX 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #16562.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS80758.

XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 46930; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 555 AA;

Query Match 12.6%; Score 100; DB 4; Length 555;
 Best Local Similarity 31.0%; Pred. No. 0.74;
 Matches 35; Conservative 10; Mismatches 48; Indels 20; Gaps 5;

QY 37 REPARSPSSLOPRHPAPRPVVKLHRLAQAQGAQGLAPVMGQPLRDGGRHS-----G 91
 DB 10 RAPPPAPRKRSRQAPLAPRP--WSSRARLPRSRPSAIPPGWG---RAGKDSAGWCAGG 64
 QY 92 PRHSGPRRTQAQLLRVGCVLGTCCVQNLISHR-----LWQLMGPAQRQDSAP 138
 DB 65 P-----APRATHAPSQQLGADGPEAVAQDTERRLGPPTALWPAERPGRGDASP 113

Search completed: October 22, 2004, 08:51:09
 Job time : 158 secs

A;Accession: C86301
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-414 <STO>
A;Cross-references: UNIPROT:Q9BEE9; GE:AE005172; NID:Y9989058; PIDN:AGI10821.1; GSPDB:GN
C;Genetics:
A;Map position: 1

Query Match	11.8%;	Score 93.5;	DB 2;	Length 414;	
Best Local Similarity	30.7%;	Pred. No. 1.6;			
Matches	42;	Conservative 13;	Mismatches 51;	Indels 31;	Gaps 7
Qy	20	PGSLRSISGGPRPVKPREPARSPSSISQRRHPAPRPVWKLHRALOAQRACAGLAPVWG	79		
Db	254	FGSPIRRRGDTF-----PRRRFA-SPSRGSPSPSPPPR-----RYRSPFRGSP-RRRG	300		
Qy	80	QPLRDGG-----RCHSGPRRHSGGPRRTQQLIRVGCVLGTQOVNLSHRLWQL	127		
Db	301	SPVARRSPFLRRSPPPRLRSPRRSPIRRRSPPIRRP-----GRSRSSISPRKGR-	355		
Qy	128	MGPAGRQDSAPVDPSPP	144		
Db	356	-GPAGRRGRSSSYSSSP	371		

RESULT 3
SI0889
proline-rich protein - human
C:Species: Homo sapiens (man)
C:Date: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: SI0889
R:Lyons, K.M.; Stein, J.H.; Smithies, O.
Genetics 120, 267-278, 1988
A:Title: Length polymorphisms in human proline-rich protein genes generated by intragenic
A:Reference number: S02127; MUID:89121440; PMID:2851479
A:Accession: SI0889
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-309 <LXO>
A:Cross-references: UNIPROT:Q04118; EMBL:X07881; NID:G35637; PIDN:CAA30728.1; PID:G296666
C:Genetics:
A:Introns: 22/1; 34/1
A:Superfamily: proline-rich protein

Query Match	11.5%;	Score 91.5;	DB 2;	Length 309;
Best Local Similarity	27.3%;	Pred. No. 1.8;		
Matches 35; Conservative 13; Mismatches 63; Indels 17; Gaps 3				
Qy	20	PGSLRSLSGGPRPVKPREPARSPSSLSLOPHHPAPRPVWKLHRAIQACAGAGLAVMG	79	
Dd	188	POGNQSQGPPRRPKGPEGP---PQGNQSQGPPRRPKPEGPSQGNGKPGRPPPHFG	244	
Qy	80	QPLRDGGRHQSGRRHSGRPTAQLLRVGCVLGTCQVNLSHLWLQMLGMPAGRODSAPV	139	
Dd	245	KPGQFPFQEGNKQRPPPPRPAQPQQPPPGG-----NPQOPLPPFAKGKCGGPPP	292	
Qy	140	DPSS--PH	145	
Dd	293	PPQGRPH	300	

RESULT 4
A36298
proline-rich protein PRB3M (null) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C:Accession: A36298
R:Azen, E.A.; Minaguchi, K.; Latreille, P.; Kim, H.S.
Am. J. Hum. Genet. 47, 686-697, 1990
A:Title: Alleles at the PRB3 locus coding for a disulfide-bonded human salivary proline
A:Reference number: A36298; MUID:91022705; PMID:2171329
A:Accession: A36298
A>Status: preliminary; not compared with conceptual translation

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A:Molecule type: DNA
A:Residues: 1-220 <AZE>
A:Cross-references: UNIPROT:Q7M4M9
C:Genetics:
  A:Gene: GDB:PRB3
  A:Cross-references: GDB:119513; OMIM:168840
  A:Map position: 12p13.2-12p13.2
  C:Superfamily: proline-rich protein

Query Match      11.5%; Score 91; DB 2; Length 220;
Best Local Similarity 30.6%; Pred. No. 1.4;
Matches 41; Conservative 7; Mismatches 66; Indels 20; Gaps 6;

Qy      18  QLPGLSRSLGGDRPVKPRPPARSSSLSQPHDPAPRPVWKLHRLQAQRGAGLAPV 77
Db      68  QPQGGNQSQGPPPRPGKPEGPP---PQGGNQSQGPPPRPGKPEGPPQGGNQSQGPPPR 124
Qy      78  MGQ---FLRDGGRGHSGPRHSG--PRRTAQLLRVGCVLGTCCQVNLSHRLWQLMGF--- 130
Db      125  PKKEGPPPPQGGNQSQGPPPHPKPEGPPQ-----GGNQSQGPPPRPKKEGPPQ 176

Qy      131  AGRQDSAPVDPSPP 144
Db      177  GGNOSQGF--PPRP 188

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RESULT 5
B55663
oligodendrocyte-specific proline-rich protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Aug-1995 #sequence_revision 09-Jul-2004
C:Accession: B55663; A55663
R:Yamamoto, Y.; Mizuno, R.; Nishimura, T.; Ogawa, Y.; Yoshikawa, H.; Fujimura, H.; Adachi, A.
J. Biol. Chem. 269, 31725-31730, 1994
A:Title: Cloning and expression of myelin-associated oligodendrocytic basic protein. A.
A:Reference number: A55663; MUID:95081123; PMID:7989345
A:Accession: B55663
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-170 <YAM>
A:Cross-references: UNIPROT:Q63327; GB:D28110; NID:G644501; PIDN:BAA05657.1; PID:d10062
A:Accession: A55663
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-68, 'RTV' <YA2>

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Query Match      11.3%; Score 90; DB 2; Length 170;
Best Local Similarity 40.3%; Pred. No. 1.4;
Matches 29; Conservative 2; Mismatches 35; Indels 6; Gaps 4;

Qy 31 PRPVKPREP--PARSPSSSTLOPRHPAPRPVVVKLHRLALQQRGAGLAPVWQQLPRLDGRQ 88
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 100 PREAKPSRPTIPAKPRSPFSRTERQPRRPEV-RPPPAKQKPPQKSKQPARSSPLRGPGTS 158
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

Qy 89 HSG-PRRHSGPR 99
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 159 RGSSEPTR--APR 168
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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RESULT 6
E30411
  synapsin Ia - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 01-Dec-2000
C:Accession: E30411; F30411; A35758
C:Suedhof, T.C.; Czernik, A.J.; Kao, H.T.; Takei, K.; Johnston, P.A.; Horiuchi, A.; Kan
  Science 245, 1474-1480, 1989
A:Title: Synapsins: mosaics of shared and individual domains in a family of synaptic ve
A:Reference number: A30411; MUID:89388265; PMID:2506642
A:Accession: E30411
A>Status: preliminary
A:Molecule type: mRNA

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Query Match	11.1%;	Score 88;	DB 2;	Length 304;
Best Local Similarity	27.8%;	Pred. No. 3.4;		
Matches	37;	Conservative	17;	Mismatches 59; Indels 20; Gaps 5
Qy	19	LPGLSLPSLGGDPPVPKPRPPA---RSPSSSLOPRHEAPRPVVMKHLRALQAQORGAGLIA	75	
Db	41	LPGLSSAATGSRCPVPRGRPPPSGARISASRWRRRPPCQSPFCWAWTHRPQGRPSG-S	99	
Qy	76	PVMGQPLRDGGRQHSRRHSIGPRRTQAQLLRVGCVLGTCCQVQNLHSLRLWLQMLGP----	130	
Db	100	PSDGLP-RTAHTSRRCPPACAQSRGRRTMKRPAC-----SRRGMPVGDPEDPAN	148	
Qy	131	AGRQDSAPVDFSS	143	
Db	149	SGLEPNPVPFRSS	161	

Query Match	11.0%;	Score 87.5;	DB 2;	Length 308;
Best Local Similarity	27.5%;	Pred. NO. 3.7;		
Matches 39;	Conservative 15;	Mismatches 39;	Indels 49;	Gaps 8
QY	22	SLRSLSGDDPRPVKPREPPASRP-SSSLQPRHPAPRPVVVKLHRLAQQRGAGLAPVMQG	80	
Db	4	SASRSDDGD--PLRPASPLRLSPVSDGDDPLRPA-----SPRLRS	41	
QY	81	PLRDGRQHSGPRRHSGPRRTQAOALLRVGCVLG-TCQVONLSHRLWLMGPPAGRODS	136	
Db	42	PVSDGG--DPLRPASP-RLRSPLGASRPVGLTAYLEQVRTGVMDI--PAGYLPADYF	94	
QY	137	-----APVDPS	143	
Db	95	EGITMAGGVAVLLPPQPVDPDES	116	

RESULT 10
S75327

A.; Azen, E.A.; Minaguchi, K.; Latreille, P.; Klm, H.S.
Am. J. Hum. Genet. 47, 686-697, 1990
A.; Title: Alleles at the PRB3 locus coding for a disulfide-bonded human salivary A; Reference number: A36238; MUID:91022705; PMID:2171339

Query Match	10.8%;	Score 86;	DB 2;	Length 383;
Best Local Similarity	27.4%;	Pred. No. 6;		
Matches 48;	Conservative 11;	Mismatches 34;	Indels 82;	Gaps 111;
Qy	11	CISLILCLQPGSLRSLSGDRPPVKPK--REPPA-RSPSSSLQPRHPAPRPVVKLHLRALQ	67	
Db	92	CPSLCPSEEPGT-----SGTEPGLPASRRPPGLRSLPSLVKPK-----E	131	
Qy	68	AQRGAGL---AP-----VMQQLPDLGGGRQSGRR-----	94	
Db	132	CLRGATLGAQAPESRGQGLRVPVRVPCQ--EGPRQGRQRPVPRFPGLQSPGCPPE	189	
Qy	95	-----HSGPRTRQALLRVGCVLGTCTQYONLSHRLWLQMLMGPAGRODSAPVDPSSP	144	
Db	190	GTLGVPSPPLOARASPSRRGASLGG-OVO--PHR-----DPSGP	225	

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